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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,586D

DATE: 07/14/2003

TIME: 10:28:45

Input Set : A:\701586

Output Set: N:\CRF4\07142003\I701586D.raw

3 <110> APPLICANT: Kock, Michael
 4 Hoeger, Thomas
 5 Kroeger, Burkhard
 6 Otterbach, Bernd
 7 Lubisch, Wilfried
 8 Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586D
 C--> 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 35
 22 <170> SOFTWARE: PatentIn/WordPerfect
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1843
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (3)...(1715)
 32 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue
 34 <400> SEQUENCE: 1

36 cc atg gcg gcg cg	47
37 Met Ala Ala Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg	
38 1 5 10 15	
40 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa	95
41 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu	
42 20 25 30	
44 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg	143
45 Asp Ser Ser Pro Ala Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser	
46 35 40 45	
48 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa	191
49 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu	
50 50 55 60	
52 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct	239
53 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala	
54 65 70 75	
56 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat	287
57 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr	
58 80 85 90 95	
60 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc	335
61 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu	

See page 6.

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62	100	105	110	
64 cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat				383
65 Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp				
66 115 120 125				
68 gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa				431
69 Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys				
70 130 135 140				
72 atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc				479
73 Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala				
74 145 150 155				
76 aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg				527
77 Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp				
78 160 165 170 175				
80 gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta				575
81 Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu				
82 180 185 190				
84 cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa				623
85 Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys				
86 195 200 205				
88 gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt				671
89 Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu				
90 210 215 220				
92 cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa				719
93 Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu				
94 225 230 235				
96 gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg				767
97 Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly				
98 240 245 250 255				
100 aag ctg aca gtc gca caa atc aag gca ggt tac cag tct ctt aag aag				815
101 Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys				
102 260 265 270				
104 att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa				863
105 Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu				
106 275 280 285				
108 gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt				911
109 Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg				
110 290 295 300				
112 act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa				959
113 Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln				
114 305 310 315				
116 tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa				1007
117 Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys				
118 320 325 330 335				
120 aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac				1055
121 Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn				
122 340 345 350				
124 cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa				1103
125 Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys				
126 355 360 365				

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128	gtg	att	tcc	cag	tac	ctt	caa	tct	acc	cat	gct	ccc	aca	cac	agc	gac		1151
129	Val	Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp		
130		370				375						380						
132	tat	acc	atg	acc	ttg	ctg	gat	ttg	ttt	gaa	gtg	gag	aag	gat	ggg	gag		1199
133	Tyr	Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu		
134		385				390						395						
136	aaa	gaa	gcc	tcc	aga	gag	gac	ctt	cat	aac	agg	atg	ctt	cta	tgg	cat		1247
137	Lys	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His		
138		400				405						410				415		
140	ggt	tcc	agg	atg	agt	aac	tgg	gtg	gga	atc	ttg	agc	cat	ggg	ctt	cga		1295
141	Gly	Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg		
142						420						425				430		
144	att	gcc	cca	cct	gaa	gct	ccc	atc	aca	ggt	tac	atg	ttt	ggg	aaa	gga		1343
145	Ile	Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly		
146		435				440						445						
148	atc	tac	ttt	gct	gac	atg	tct	tcc	aag	agt	gcc	aat	tac	tgc	ttt	gcc		1391
149	Ile	Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala		
150		450				455						460						
152	tct	cgc	cta	aag	aat	aca	gga	ctg	ctg	ctc	tta	tca	gag	gta	gct	cta		1439
153	Ser	Arg	Leu	Lys	Asn	Thr	Gly	Leu	Leu	Leu	Leu	Ser	Glu	Val	Ala	Leu		
154		465				470						475						
156	ggt	cag	tgt	aat	gaa	cta	cta	gag	gcc	aat	cct	aag	gcc	gaa	gga	ttg		1487
157	Gly	Gln	Cys	Asn	Glu	Leu	Leu	Glu	Ala	Asn	Pro	Lys	Ala	Glu	Gly	Leu		
158		480				485						490				495		
160	ctt	caa	ggg	aaa	cat	agc	acc	aag	ggg	ctg	ggc	aag	atg	gct	ccc	agt		1535
161	Leu	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser		
162						500						505				510		
164	tct	gcc	cac	ttc	gtc	acc	ctg	aat	ggg	agt	aca	gtg	cca	tta	gga	cca		1583
165	Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro		
166		515				520						525						
168	gea	agt	gae	aca	gga	att	ctg	aat	cca	gat	ggt	tat	acc	ctc	aac	tac		1631
169	Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr		
170		530				535						540						
172	aat	gaa	tat	att	gta	tat	aac	ccc	aac	cag	gtc	cgt	atg	cgg	tac	ctt		1679
173	Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu		
174		545				550						555						
176	tta	aag	gtt	cag	ttt	aat	ttc	ctt	cag	ctg	tgg	tga	atgttgatat					1725
177	Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp							
178		560				565						570						
180	taaataaacc	agagatctga	tcttcaagca	agaaaataag	cagtgttgta	cttgtgtatt												1785
182	ttgtgtatatt	ttatgtataa	aaaactgtac	aggctaaaaa	aaaaaaaaaa	aaaaaaaaaa												1843
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186	<211>	LENGTH:	570															
187	<212>	TYPE:	PRT															
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192	Met	Ala	Ala	Arg	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala	
193		1				5					10			15				
195	Leu	Asn	Glu	Ser	Lys	Arg	Val	Asn	Asn	Gly	Asn	Thr	Ala	Pro	Glu	Asp		

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196	20	25	30
198	Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys		
199	35	40	45
201	Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp		
202	50	55	60
204	Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala Pro		
205	65	70	75
207	80	85	90
208	Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys		
210	95	100	105
211	Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln		
213	110	115	120
214	Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala		
216	125	130	135
217	Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met		
219	140	145	150
220	Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys		
222	160	155	165
223	Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu		
225	175	165	170
226	Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln		
228	190	180	185
229	Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Thr Lys Lys Glu		
231	205	195	200
232	Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg		
234	220	210	215
235	240	225	230
237	255	245	250
238	Glu		
240	Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile		
241	270	260	265
243	Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala		
244	285	275	280
246	290	280	295
247	300	290	295
249	320	305	310
252	335	325	330
253	350	340	345
255	365	355	360
258	380	370	375
261	380	370	375
262	400	385	390
264	415	385	405
267	Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly		
268	410	405	410

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270	Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg	Ile	
271			420					425								430	
273	Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	Ile	
274		435						440							445		
276	Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala	Ser	
277			450					455							460		
279	Arg	Leu	Lys	Asn	Thr	Gly	Leu	Leu	Leu	Ser	Glu	Val	Ala	Leu	Gly		
280	465			470					475						480		
282	Gln	Cys	Asn	Glu	Leu	Leu	Glu	Ala	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Leu	
283									490						495		
285	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser	Ser	
286									505						510		
288	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro	Ala	
289									520						525		
291	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr	Asn	
292									535						540		
294	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu	Leu	
295	545					550				555						560	
297	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp							
298						565				570							
301	<210>	SEQ	ID	NO:	3												
302	<211>	LENGTH:	2265														
303	<212>	TYPE:	DNA														
304	<213>	ORGANISM:	Homo sapiens														
306	<220>	FEATURE:															
307	<221>	NAME/KEY:	CDS														
308	<222>	LOCATION:	(242)...(1843)														
309	<223>	OTHER INFORMATION:	product is Poly ADP Ribose Polymerase; from uterus tissue														
311	<400>	SEQUENCE:	3														
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315	tagccatgt	ctaatcccc	acacaagctc	atccccggcc	tctggattg	ttgggaattc										120	
317	tctccctaat	tcacgcctga	ggctcatgga	gagttgctag	acctggact	gccctggag										180	
319	gcgcacacaa	ccaggccggg	tggcagccag	gacctctccc	atgtccctgc	ttttcttggc										240	
321	c	atg	gct	cca	aag	ccg	aag	ccc	tgg	gta	cag	act	gag	ggc	cct	gag	286
322	Met	Ala	Pro	Lys	Pro	Lys	Pro	Trp	Val	Gln	Thr	Glu	Gly	Pro	Glu		
323	1				5				10						15		
325	aag	aag	ggc	cg	c	g	a	gg	g	g	g	ac	ccc	ttc	cgc	tcc	334
326	Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	Ser	
327									20			25			30		
329	acc	gct	gag	gcc	ctc	aag	gcc	ata	ccc	gca	gag	aag	cgc	ata	atc	cgc	382
330	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile	Arg	
331									35			40			45		
333	gtg	gat	cca	aca	tgt	cca	ctc	agc	agc	aac	ccc	ggg	acc	cag	gtg	tat	
334	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val	Tyr	430
335									50			55			60		
337	gag	gac	tac	aac	tgc	acc	ctg	aac	cag	acc	aac	atc	gag	aac	aac	aac	
338	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	Asn	
339									65			70			75		
341	aac	aag	ttc	tac	atc	atc	cag	ctg	ctc	caa	gac	agc	aac	cgc	ttc	tcc	526

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,4,5,6,7,9,10,11
Seq#:12; Xaa Pos. 1,2,6,7,9,10,11,12,13,14,16,17,18
Seq#:13; Xaa Pos. 6,7,8,9,10,11,12,13,16,17,21,22,24,25,26,27,28,29,31,32
Seq#:13; Xaa Pos. 33,41,42,43,48
Seq#:14; Xaa Pos. 1,2,3,4,5,6,7,9,10,11,12,13,14,16,17,18,19,20,21
Seq#:15; Xaa Pos. 2,3,4,5,6,7,8,9,10,12,13,15,16,20,21,22,23,24,25,26,27,28
Seq#:15; Xaa Pos. 29,30,31,32
Seq#:16; Xaa Pos. 2,3,4,6,8,9,10,11,14,16,18,19,20,21,22,24,25,26,28
Seq#:17; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43
Seq#:18; Xaa Pos. 4,8,11,12,13
Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16
Seq#:20; Xaa Pos. 2,3,4,6
Seq#:21; Xaa Pos. 2,3,5,6,7,8,10,11,12,14,15,16,17,18,19,20,21,22,24,26,27
Seq#:22; Xaa Pos. 2,3,4,6,7,8,10,11,12,13
Seq#:29; Xaa Pos. 2,3,4
Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:30; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,36,37
Seq#:34; Xaa Pos. 36,48,51,52,53,57,68,72,74,80,85,89,92,106,122,126,147
Seq#:34; Xaa Pos. 156,160,173,177,189,191,202,205,212,226,242,245,275,277
Seq#:34; Xaa Pos. 280,291,302,304,313,332,336,337,338,340,342,370,385,393
Seq#:34; Xaa Pos. 404,467,470,475,492,493,540,543,545,558,575

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
M:341 Repeated in SeqNo=12
L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:1497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14
L:1524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15
L:1549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:1576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:1620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
M:341 Repeated in SeqNo=21
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
M:341 Repeated in SeqNo=30
L:1897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:32
M:341 Repeated in SeqNo=34